

From stability to dynamics:

Bending, David; Ono, Masahiro

DOI:

[10.1111/cei.13194](https://doi.org/10.1111/cei.13194)

License:

Other (please specify with Rights Statement)

Document Version

Peer reviewed version

Citation for published version (Harvard):

Bending, D & Ono, M 2018, 'From stability to dynamics: understanding molecular mechanisms of regulatory T cells through *Foxp3* transcriptional dynamics', *Clinical & Experimental Immunology*.
<https://doi.org/10.1111/cei.13194>

[Link to publication on Research at Birmingham portal](#)

Publisher Rights Statement:

This is the peer reviewed version of the following article: Bending, D. and Ono, M. (2018), From stability to dynamics: understanding molecular mechanisms of regulatory T cells through *Foxp3* transcriptional dynamics. *Clin Exp Immunol*. Accepted Author Manuscript. doi:10.1111/cei.13194, which has been published in final form at 10.1111/cei.13194. This article may be used for non-commercial purposes in accordance with Wiley Terms and Conditions for Self-Archiving.

General rights

Unless a licence is specified above, all rights (including copyright and moral rights) in this document are retained by the authors and/or the copyright holders. The express permission of the copyright holder must be obtained for any use of this material other than for purposes permitted by law.

- Users may freely distribute the URL that is used to identify this publication.
- Users may download and/or print one copy of the publication from the University of Birmingham research portal for the purpose of private study or non-commercial research.
- User may use extracts from the document in line with the concept of 'fair dealing' under the Copyright, Designs and Patents Act 1988 (?)
- Users may not further distribute the material nor use it for the purposes of commercial gain.

Where a licence is displayed above, please note the terms and conditions of the licence govern your use of this document.

When citing, please reference the published version.

Take down policy

While the University of Birmingham exercises care and attention in making items available there are rare occasions when an item has been uploaded in error or has been deemed to be commercially or otherwise sensitive.

If you believe that this is the case for this document, please contact UBIRA@lists.bham.ac.uk providing details and we will remove access to the work immediately and investigate.

Title: From stability to dynamics: understanding molecular mechanisms
of regulatory T cells through *Foxp3* transcriptional dynamics

Authors: David Bending^{1, 2} and Masahiro Ono^{2*}

Affiliations

¹Institute of Immunology and Immunotherapy, College of Medical and Dental
Sciences, University of Birmingham, B15 2TT, United Kingdom.

²Department of Life Sciences, Faculty of Natural Sciences, Imperial College
London, Sir Alexander Fleming Building, Imperial College Road, London, SW7
2AZ, United Kingdom

* Correspondence to: Dr Masahiro Ono, Department of Life Sciences, Sir
Alexander Fleming Building, Imperial College Road, South Kensington, London,
SW7 2AZ, United Kingdom. E-mail address: m.ono@imperial.ac.uk

Short title: *Foxp3* transcriptional dynamics in regulatory T cells

Key words: *Foxp3*, regulatory T cells (Treg), Nr4a3, transcriptional
autoregulatory circuit, Time of cell kinetics and activity (Tocky),

Abbreviations: regulatory T cells (Treg); Timer of cell kinetics and activity
(Tocky); T cell receptor (TCR); interleukin (IL); fluorescent protein (FP);
conserved non-coding sequences (CNS); double-positive (DP); knock out (KO);
Treg-specific demethylated region (TSDR); chromatin conformation capture
(3C).

Summary

Studies on regulatory T cells (Treg) have focused on thymic Treg as a stable lineage of immunosuppressive T cells, the differentiation of which is controlled by the transcription factor *Foxp3*. This lineage perspective, however, may constrain hypotheses regarding the role of *Foxp3* and Treg in vivo, particularly in clinical settings and immunotherapy development. In this review, we synthesise a new perspective on the role of *Foxp3* as a dynamically expressed gene, and thereby revisit the molecular mechanisms for the transcriptional regulation of *Foxp3*. Particularly, we introduce a recent advancement in the study of *Foxp3*-mediated T cell regulation through the development of the Timer of cell kinetics and activity (Tocky) system and show that the investigation of *Foxp3* transcriptional dynamics can reveal temporal changes in the differentiation and function of Treg in vivo. We highlight the role of *Foxp3* as a gene downstream of T cell receptor (TCR) signalling and show that temporally-persistent TCR signals initiate *Foxp3* transcription in self-reactive thymocytes. In addition, we feature the autoregulatory transcriptional circuit for the *Foxp3* gene as a mechanism for consolidating Treg differentiation and activating their suppressive functions. Furthermore, we explore the potential mechanisms behind the dynamic regulation of epigenetic modifications and chromatin architecture for *Foxp3* transcription. Lastly, we discuss the clinical relevance of temporal changes in the differentiation and activation of Treg.

Introduction: Dynamics of *Foxp3* transcription as a key to understanding regulatory T cell-mediated immune regulation

It is widely considered that regulatory T cells (Treg) constitute a distinct lineage of CD4⁺ T cells dedicated for immunosuppression [1]. Key evidence for the distinct lineage include: (i) Treg development is controlled by the transcription factor *Foxp3* [2]; and (ii) the development of Treg in the thymus is delayed to after that of other T cells under physiological conditions [3]. However, accumulating evidence show the simultaneous development of Treg and other T cells [4, 5] and Treg plasticity is now widely recognised as Treg can lose *Foxp3* expression and become effector T cells (ex-Treg) during inflammation [6, 7]. Thus, studies on dynamic changes in the differentiation and activation status of Treg – and other T cells – in vivo is essential for understanding *Foxp3*-mediated T cell regulation. This dynamic perspective is important for not only basic research but also clinical research and immunotherapy development, which is illustrated by the catastrophic clinical trial of the superagonistic anti-CD28 antibody TGN1412 in 2006.

TGN1412 was developed as an immunosuppressive treatment, after an anti-CD28 antibody was found to suppress autoimmune reactions in rodent models [8]. TGN1412 was thus designed to bind to the CD28 molecule on the surface of Treg, which would theoretically in turn suppress non-Treg [9]. This trial, however, resulted in catastrophe where all 6 volunteers given TGN1412 developed a 'Cytokine Storm' due to stimulation of a significant proportion of T cells [10]. Later, it was found that CD28 molecules in memory-phenotype T

1 cells are downregulated in primates – which does not occur in humans – and
2 this species difference was deemed to be the major cause of the incident [11].
3 Meanwhile, Vitetta and Ghetie pointed out that Treg and non-Treg may not
4 represent strictly separate lineages, and therefore the assumption of specific
5 activation of Treg may have been inappropriate [12]. In fact, basic studies later
6 showed the plasticity of Treg: Treg may lose Foxp3 expression during
7 inflammation and non-Treg may acquire Foxp3 expression [13]. Summarizing,
8 the case provides two important lessons: first, the concepts of lineage stability
9 may constrain hypotheses, which can be detrimental in clinical settings; second,
10 it is fundamental to investigate the dynamic changes in the differentiation and
11 activation statuses of Treg and other T cells in vivo, which are still poorly
12 understood.

13
14 The key evidence of Foxp3 as the lineage-specification transcription factor is
15 that mutations in the *Foxp3/FOXP3* gene can lead to autoimmune disease in
16 both mice [14] and humans [15]. However, this does not preclude the dynamic
17 induction of Foxp3 as a negative regulator in response to T cell activation. In
18 fact, FOXP3 expression can be induced solely by T cell receptor (TCR) signals
19 in human T cells [16], and although less efficiently, in mice as well [17], and the
20 induction is enhanced by TGF- β and interleukin (IL)-2 [18]. TGF- β is produced
21 by activated antigen presenting cells such as dendritic cells [19] and
22 macrophages [20], while IL-2 is mainly produced by activated T cells,
23 particularly CD4⁺ T cells [21]. Since the immunosuppressive Treg population is
24 commonly identified by the expression of Foxp3 (as Foxp3⁺ T cells in mice [2],

and FOXP3^{high}CD45RA⁺ [22, 23] or FOXP3⁺CD127⁻CD25^{high} T cells [24, 25] in humans), the investigation of *Foxp3* dynamics in vivo, especially during immune responses, will be key for understanding the in vivo dynamics of Treg and T cell regulation. To this end, we have recently developed a new technology **Timer of cell kinetics and activity** (Tocky) system, which allows the investigation of in vivo dynamics of Foxp3 and Treg during physiological immune responses [26, 27].

In this article, we will aim to introduce a dynamic perspective to the molecular mechanisms that account for the transcriptional and epigenetic control of the *Foxp3* gene, and thereby to improve the understanding of Foxp3-mediated T cell regulation in vivo.

Development of Timer of cell kinetics and activity (Tocky) for investigating in vivo dynamics of Treg differentiation

The current understanding of Treg differentiation and function is significantly based on evidence obtained by Foxp3 fluorescent protein (FP) reporters (such as EGFP [28, 29]) and fate mapping systems for the *Foxp3* gene (e.g. *Foxp3*^{CreGFP}: *Rosa26*^{RFP} [17] and *Foxp3*^{ERT2CreGFP}:*Rosa26*^{YFP} [30]). Notably, all these systems rely on stable FPs such as GFP, the half-life of which is longer than 56 hours. Therefore, temporal changes in *Foxp3* transcription shorter than 2 – 3 days cannot be investigated by these reporter systems.

In order to understand in vivo dynamics of those molecular mechanisms underlying the differentiation and function of Treg, we have recently developed the Tocky system using Fluorescent Timer protein (Timer). Timer proteins exhibit a short-lived blue fluorescent form, before maturation to the stable red state [27, 31]. The half-life of blue fluorescence is ~ 4 hours [26, 27], and that of the mature red fluorescence is ~ 5 days [26]. Thus, blue and red fluorescence (Blue and Red) provide a measurement of both the 'real-time' activity and the history of gene transcription [26]. Tocky uses this information to quantitatively analyse dynamic changes in transcriptional activities during cellular activation and differentiation [27]. Importantly, we have identified three characteristic dynamics of transcription in the Tocky system: Blue⁺Red⁻ cells are those that have just initiated transcription (New); Blue⁺Red⁺ cells along the diagonal line between Blue and Red axes are those with sustained transcription, accumulating both blue and red form proteins (Persistent); and Blue⁻Red⁺ cells are those that have recently downregulated gene expression under the detection threshold of flow cytometry and are inactive in transcription of the gene (Arrested or Inactive) [27] (**Figure 1**).

Foxp3 transcription is controlled mainly by 5' upstream sequences and conserved non-coding sequences (CNS) 1-3 in intronic regions [7, 32-34]. Importantly, while TCR signals (together with TGF- β and IL-2 signals) induce *Foxp3* expression in any T cells in vitro [18], naturally-arising *Foxp3* expression is found mostly in self-reactive T cells in non-inflammatory conditions [1]. Thus, we will classify the mechanisms for *Foxp3* transcription into two groups:

(i) Mechanisms for the activation of *Foxp3* transcription: these are used during thymic Treg selection and peripheral Treg differentiation and are potentially involved in the mechanism for tonic TCR signal-mediated activation of *Foxp3* transcription.

(ii) Mechanisms for the consolidation and tuning of *Foxp3* transcription: these are used for sustaining *Foxp3* transcription over time, which induces effector Treg differentiation and the dynamic regulation of epigenetic modifications, such as demethylation of CpG islands in enhancer regions (**Figure 2**).

Mechanisms for the activation of *Foxp3* transcription

Foxp3 as a TCR signal downstream gene

The differentiation and function of Treg is under the control of TCR signals [35-38]. In the thymus, the recognition of cognate antigen induces not only negative selection but also the differentiation of CD25⁺Foxp3⁺ Treg from CD4-SP cells using transgenic TCR systems [39-41]. On the other hand, TCR transgenic mice in the Recombination activating gene (*Rag*) deficient backgrounds lack Foxp3⁺ T cells due to the absence of self-antigen presentation [42, 43]. The analysis of TCR signals using reporter mice have provided insights into the mechanism for TCR-mediated Treg differentiation. The Hogquist group showed that Treg receive strong TCR signals in the thymus and the periphery, when analysed using a Nur77(Nr4a1)-GFP transgenic reporter [44]. Using Nr4a3-Tocky, we have shown that Foxp3 expression in the thymus occurs in T cells that have received temporally persistent TCR signals [27]. Furthermore, using

1 Foxp3-Tocky we showed that *Foxp3* transcription is initiated in non-Treg cells
2 during inflammation in the periphery [26]. In humans, activation-induced FOXP3
3 in conventional T cells suppresses their proliferation and cytokine production in
4 a cell intrinsic manner [45]. In addition, activated conventional T cells can
5 express both Foxp3 and CTLA-4 and thereby acquire the suppressive function
6 that is dependent on CTLA-4 [46]. These suggest that Foxp3 has a role in
7 negative feedback regulation of T cell activation in cooperation with other
8 immunoregulatory molecules, including CTLA-4. *Foxp3* transcription, therefore,
9 is thus under the control of TCR signals in both the thymus and the periphery. In
10 addition, in normal homeostasis, Treg and naturally-arising memory-phenotype
11 T cells are self-reactive and receive 'tonic' TCR signals in the periphery [27, 44].
12 Considering this evidence, the biological meaning of TCR signal-induced Foxp3
13 expression includes two situations: (i) antigen recognition-induced *Foxp3*
14 transcription in Foxp3⁻ cells (conventional T cells; non-Treg) in the thymus and
15 the periphery; and (ii) the effects of tonic TCR signals in Foxp3⁺ Treg.

16 In line with the evidence of Foxp3 expression upon TCR stimulation, the gene
17 regulatory regions of the *Foxp3* gene are bound by transcription factors
18 downstream of major branches of the TCR signalling pathway, including NFAT
19 and AP1 [47], the NF- κ B components c-Rel and p65 [32, 48-50], Cyclic AMP
20 response element-binding protein (CREB) [51], and Nr4a proteins [52] (**Figure**
21 **2**).

22 Nr4a proteins (Nr4a1, Nr4a2, and Nr4a3) bind to their target sequences as
23 homodimers or heterodimers and regulate transcription [53, 54]. Foxp3⁺ Treg

1 differentiation is abolished in Nr4a1/2/3 triple knock out (KO) and Nr4a1/3
2 double KO, and these mice develop fatal autoinflammatory disease [52]. Nr4a
3 proteins bind to the *Foxp3* promoter upon anti-CD3 stimulation [52], and
4 retroviral gene transduction of Nr4a2 or Nr4a3 induces *Foxp3* transcription [55].
5 Importantly, however, Nr4a triple KO lack not only Foxp3⁺ Treg but also most of
6 double-positive (DP) cell population [52], which suggests that the Treg reduction
7 in these KO mice is a consequence of defective regulation of positive and
8 negative selection. Meanwhile, we have identified *Nr4a3* as the gene that is the
9 most correlated with the effects of TCR signals in the thymus and the periphery,
10 followed by *Nr4a1* [27]. Specifically, using Canonical Correspondence Analysis
11 (CCA) [56], we analysed the transcriptome dataset of thymic T-cell populations
12 and that of resting and anti-CD3 stimulated peripheral T cells, and thereby
13 identified the genes that were correlated with both thymic T-cells under
14 selection (in vivo TCR signals) and peripheral T cell activation [27]. By
15 developing Nr4a3-Tocky, we have shown that temporally persistent TCR
16 signals sustain *Nr4a3* transcription and initiate *Foxp3* transcription [27]. This
17 leads to the new model for Nr4a that the recognition of cognate antigen conveys
18 persistent TCR signals, which induce and accumulate Nr4a proteins and
19 thereby control thymic selection and differentiation processes including Treg
20 differentiation.

21
22 *Foxp3* transcription-enhancing cytokine signals

Foxp3 transcription is activated by IL-2 signalling in the presence of TCR stimulation and TGF- β signalling [18]. It is, however, unknown whether these cytokine signals can regulate *Foxp3* transcription independently from TCR signalling.

IL-2 signalling is a central cytokine for T cell activation, proliferation and differentiation [21]. The expression of CD25 (IL-2R α -chain) is induced by TCR and CD28 signals and forms the high-affinity IL-2R together with IL-2R β -chain (CD122) and the common γ -chain (CD132) [57, 58]. IL-2 binding to IL-2R triggers phosphorylation of Stat5 by the associated kinases Jak1 and Jak3, which promotes cell cycle entry and proliferation of TCR stimulated T cells [59].

In addition to the role in T cell activation, CD25 is a surface marker for Treg mice [60] and humans as well [61]. In fact, IL-2 signalling is functional in Treg. Phosphorylated Stat5 binds to the promoter and CNS2 and activates *Foxp3* transcription [62, 63]. KO mice for the genes that are involved in IL-2 signalling (*Il2* [64], *Il2ra* [64], *Il2rb* [65], *Jak3* [66], and *Stat5a* / *Stat5b* [67]) have reduced *Foxp3*⁺ T-cells in the thymus and periphery. Thus, IL-2 signalling is required for the activation of *Foxp3* transcription, most probably both during an early phase of Treg differentiation as well as the maintenance of both *Foxp3* transcription and the Treg population. Considering the primary role of IL-2 for the activation and proliferation of T cells [21], this suggests a role of *Foxp3* as a sensor for the IL-2 abundance in the environment surrounding individual T cells. In other words, when T cells are activated, IL-2 becomes abundant, which enhances *Foxp3* expression in nearby T cells. Given that IL-2R expression in Treg absorbs IL-2 and suppresses IL-2-mediated T cell proliferation [68], the size of

the T cell population may be self-regulated through the feedback mechanism involving IL-2, CD25, and Foxp3 [38].

TGF- β signalling has multifaceted effects on tissue development and regeneration, inflammation, and cancer in a context dependent manner [69].

The importance of TGF- β signalling in T cells is recognised particularly in mucosal and tumour immunity [70]. The transcriptional response of T cells to TGF- β signalling is also context-dependent and is illustrated by the reciprocal differentiation of Th17 and Treg by IL-6 and IL-2, respectively, under the presence of TGF- β [71, 72]. TGF- β signal-activated Smad3 binds to the CNS1 of the *Foxp3* gene [32, 73]. However, the genetic deletion of the Smad-binding site does not change the frequencies of Treg in the thymus and the periphery, apart from marginal reductions of Foxp3⁺ T cells in Peyer's patches and Lamina Propria in aged mice [74]. This suggests that TGF- β controls *Foxp3* transcription through multiple sites in the *Foxp3* gene and/or through the induction of other factors. While IL-2 signalling is intrinsically required for Treg differentiation as discussed above, the opposing effects of IL-6 signalling seem to be reactive and inflammation-dependent, as the genetic deletion of *Stat3* does not affect Treg populations, while inhibiting the differentiation of Treg in the CD45RB^{hi} T cell-mediated colitis model [75].

Veldhoen and Stockinger have proposed the model that TGF- β skews CD4⁺ T-cell differentiation from Th1 to Th17 [76], and as such, TGF- β may shift T cells from the Th1-Th2 axis to the Th17-Treg axis. In TGF- β -rich microenvironment, such as in the intestines, tumour, or destructed tissues with regeneration and

remodelling, the persistence of pathogen or autoantigen may activate monocytes and dendritic cells, and thereby repress *Foxp3* transcription and promote Th17 differentiation, as observed in rheumatoid arthritis patients [77]. In contrast, once the activation of innate immune cells is terminated, *Foxp3* transcription may be initiated in antigen-reactive T cells, as observed by Foxp3-Tocky [26], especially when adjacent T cells are proliferating and producing IL-2, inducing the resolution of inflammation.

Mechanisms for the consolidation and tuning of *Foxp3* transcription – the role of autoregulatory transcriptional circuit for the *Foxp3* gene

The maintenance of *Foxp3* transcription in Treg requires CNS2, which includes the widely studied Treg-specific demethylated region, TSDR [33]. The CpG motifs in the TSDR are methylated in non-Treg cells, and fully demethylated in thymic Treg [22, 33]. The genetic deletion of CNS2 results in the reduction of *Foxp3* expression in thymic Treg but does not affect *Foxp3* induction in vitro [32]. CNS2 is bound by several key transcription factors, including the Runx/Cbf- β complex [78-81], Ets-1 [82], which makes an active complex with Runx1 [83], *Foxp3* protein [32], and Stat5 [63].

Foxp3 binding to CNS2 is dependent on Runx1/CBF- β [32]. Importantly, the expression of *Foxp3* in Treg is reduced in both CBF- β -deficient Treg [78] and CNS2-deleted Treg [34]. CNS2 is required for maintaining the number of Treg in the periphery during homeostasis and is also important for sustaining *Foxp3* expression during inflammation [7, 34]. CNS2-deleted Treg lose *Foxp3*

1 expression in the presence of proinflammatory cytokines, including IL-4 and IL-
2 6, and become effector T cells to enhance autoimmune inflammation in mice [7].
3 Furthermore, analysis of TCR repertoires in human Treg also suggests the
4 dynamic regulation of both CD25 and Foxp3 on T-cells in rheumatoid arthritis
5 [84]. These data together suggest that, although Foxp3 expression is commonly
6 recognised to be stable, it is in fact dynamically regulated in Foxp3⁺ Treg during
7 homeostasis and during immune responses.

8 Our recent investigations using Foxp3-Tocky have shown that, intriguingly,
9 resting Treg have intermittent *Foxp3* transcription, while activated effector Treg
10 with high expression of immunoregulatory molecules (including CTLA-4 and IL-
11 10) have more sustained *Foxp3* transcription across time [26]. The phenotype
12 of these effector Treg with temporally-persistent *Foxp3* transcription is in fact
13 very similar to those of the effector Treg that are dependent on *Myb* [85] and the
14 CD44^{hi}CD62L^{lo} activated Treg that are dependent on TCR signals [35], which
15 supports the model that TCR signals induce temporally persistent *Foxp3*
16 transcription and thereby enhance the suppressive phenotype of Treg.

17 Furthermore, by analysing female mice with heterozygosity for a hypomorphic
18 Foxp3 mutant (namely, *Scurfy* mutation), Foxp3 protein sustains the temporally-
19 persistent *Foxp3* transcriptional dynamics that promote effector Treg functions
20 [26]. In the thymus, the active demethylation of the TSDR occurs only after the
21 initiation of *Foxp3* transcription and when *Foxp3* transcription is highly sustained
22 over time [27]. These indicate that Foxp3 protein and the *Foxp3* gene form an
23 autoregulatory loop that consolidates the Treg-type TSDR demethylation during
24 thymic differentiation [27], and tunes *Foxp3* transcriptional activities and thereby

1 activates their suppressive activity during inflammation [26]. Given the critical
2 roles of the Runx1/ Cbfb complex in the maintenance of Foxp3 expression and
3 the Foxp3-Runx1 interaction in Treg differentiation and function, it is plausible
4 that this autoregulatory transcriptional circuit is formed via the binding of Foxp3-
5 Runx1/Cbfb complex [32] to CNS2 of the *Foxp3* gene (**Figure 2**).

6

7 **Dynamic regulation of epigenetic modifications and chromatin**

8 **architecture of the *Foxp3* gene**

9 TCR-induced *Foxp3* transcriptional activities can be opposed by epigenetic
10 mechanisms for silencing *Foxp3* transcription. The SUMO E3 ligase Pias3 binds
11 to the *Foxp3* promoter, and *Pias1* KO mice have increased frequencies of
12 Foxp3+ cells in CD4+ T cells, and reduced methylation of histone H3 at Lys9
13 (H3K9), which is a hallmark of repressed genes [86]. The DNA
14 methyltransferase Dnmt1 and the high mobility group transcription factors Tcf1
15 and Lef1 constitutively repress *Foxp3* transcription in CD8+ T cells, as *Dnmt1*^{-/-}
16 or *Tcf1*^{-/-} *Lef1*^{-/-} double KO permits the differentiation of Foxp3+CD8+ T cells,
17 which are rarely found in normal mice [87, 88]. In addition, the induction of
18 Foxp3 expression in *Dnmt1*^{-/-} T does not require TGF-β [87], suggesting that
19 TGF-β likely modulates epigenetic mechanisms in normal mice. Strong TCR
20 signalling in vitro causes the accumulation of Dnmt1 at the *Foxp3* promoter,
21 which can lead to increased CpG methylation and inhibition of *Foxp3*
22 transcription [89]. Thus, TGF-β may be important for tuning Dnmt1 expression
23 during T cell activation.

Foxp3-Tocky has shed light on the dynamics of *Foxp3* epigenetic regulation following the initiation of *Foxp3* transcription. Importantly, *Foxp3* transcription precedes the demethylation of TSDR in the thymus. Both thymic new *Foxp3* expressors, which are identified by Tocky [27], and immature CD24^{hi}Foxp3⁺CD4SP by Foxp3-EGFP mice [90] have fully methylated TSDR. The active process for TSDR demethylation occurs only after *Foxp3* transcription is sustained over time and the Foxp3 autoregulatory loop is formed [26]. Collectively, the interactions between Foxp3-inducing and inhibiting factors occur during the early phase of Treg differentiation when the *Foxp3* gene is still 'silenced', and we would therefore hypothesise that Foxp3 protein may also have roles in dynamically regulating the epigenetic modifications of the *Foxp3* gene. Future studies could therefore address the role of Foxp3 in the dynamic regulation of chromatin architecture, which can be investigated by chromatin conformation capture (3C) and derivative methods (e.g. Hi-C). For example, the Zheng group showed that, using 3C, NFAT activation induces the interaction of the TSDR-containing CNS2 with the *Foxp3* promoter, which facilitates enhanced *Foxp3* transcription [34]. Using Hi-C and CRISPR-mediated mutation, the Zhao group showed that the MLL family methyltransferase MLL4 binds to - 8.5k upstream enhancer of the *Foxp3* gene, and makes a chromatin loop to promote the monomethylation of histone H3 at Lys4 (H3K4me1) in the promoter and CNS3, which activates *Foxp3* transcription [91]. The chromatin organising factor Satb1 is also involved in activating *Foxp3* transcription in the thymus, as the genetic deletion of Satb1 results in the marked reduction of Foxp3⁺ Treg and the accumulation of thymic CD25⁺Foxp3⁻ Treg precursors with reduced

enhancer activity (which are identified by acetylation of histone H3 at Lys27 (H3K27ac)) [92]. Thus, it is likely that chromatin remodelling of the *Foxp3* gene underlies the temporally dynamic *Foxp3* autoregulatory loop, suggesting that the former is also dynamically induced through the interactions between Foxp3 protein and key chromatin organisers and epigenetic regulators. In addition, since those chromatin organisers and epigenetic regulators control not only the *Foxp3* gene but also other genes, the chromatin remodelling of Foxp3-target genes may be also dynamically induced in activated Treg and differentiating Treg. Future studies, therefore, should investigate the role of Foxp3 protein and its cofactors in the temporally dynamic regulation of chromatin structure within and outside the *Foxp3* gene region.

Dynamic Foxp3 expression in vivo: perspectives for basic immunology and clinical relevance

After the emergence of single cell technologies and the Tocky tool, studies on T cell regulation are shifting from the stability and plasticity of Treg to the investigation of temporal changes in Foxp3-mediated mechanisms in vivo. Our analysis of Treg in peripheral immune compartments show that, in the non-inflammatory conditions, *Foxp3* transcription is most likely modelled by intermittent gene activity [26]. This intermittent transcription may offer an explanation for the low frequency of Treg cells with detectable *Foxp3* transcripts in Treg cells analysed by single cell RNA-seq [93, 94], although these datasets have limitations due to shallow sequencing depths. Given that the temporal changes in *Foxp3* transcription control Treg function and effector Treg

1 differentiation, future work will investigate the molecular mechanisms that
2 control the real-time transcribing of the *Foxp3* gene, which can be analysed by
3 the Tocky system. In addition, in line with the temporally dynamic regulation of
4 *Foxp3* transcription in vivo, the significance of thymic and peripheral Treg
5 markers needs to be re-addressed. Our investigation using Foxp3-Tocky has
6 confirmed that the expression of Neuropilin 1 [95] and Helios [96] are
7 dynamically regulated in Treg according to *Foxp3* transcription dynamics [26],
8 and therefore are not faithful markers of thymic Treg, as has been previously
9 noted in the literature [97].

10 Importantly, clinical studies and immunotherapy development may be benefitted
11 by the endorsement of the dynamic perspective. Whether targeting Treg or not,
12 immunotherapy may dynamically change *Foxp3* transcription. If these dynamic
13 responses are clarified, immunotherapy targeting T cells may be better
14 designed with a more tailored strategy, as we recently showed by manipulating
15 *Foxp3* transcriptional dynamics through targeting inflammation-reactive effector
16 Treg by OX40 and TNFRII, which are specifically expressed in Treg with
17 temporally-persistent *Foxp3* transcription [26]. We therefore envisage that the
18 investigation of dynamic changes in molecular mechanisms during T cell
19 responses in vivo will improve the predictability of preclinical studies and
20 thereby contribute to the development of new immunotherapies for autoimmune
21 and cancer patients.

22 23 24 **Acknowledgements**

1 D.B. is funded by a University of Birmingham Fellowship. M.O. is a David Phillips
2 Fellow (BB/J013951/2) from the Biotechnology and Biological Sciences
3 Research Council (BBSRC). The authors declare that no conflicts of interest exist
4 in relation to this manuscript.

5

6

Figure Legends

Figure 1: Comparison of Tools to investigate *Foxp3*-expressing T-cells in vivo.

(A) Most *Foxp3* reporter mice use stable Fluorescent Proteins (FP), such as EGFP, the half-life of which is > 56 hours. (B) *Foxp3* fate mappers such as *Foxp3^{GFPCre}:Rosa26^{RFP}* allow the identification of Treg with *Foxp3* expression and ex-Treg that lost *Foxp3* expression. Notably, both GFP and RFP are stable FPs. (C) *Foxp3*-Tocky uses Fluorescent Timer, the emission spectrum of which spontaneously and irreversibly changes from blue to red fluorescence. The half-life of blue fluorescence is ~4 hours, and thus reports the 'real-time' activity of *Foxp3* transcription. In contrast, the half-life of red fluorescence is ~120 hours and thus reports the history of *Foxp3* transcription. The Tocky system combines Blue and Red fluorescence data and identifies characteristic transcriptional dynamics including New, Persistent, and Arrested (inactive).

Figure 2: Activation vs. consolidation and tuning of *Foxp3* transcription

We propose to classify *Foxp3* transcriptional regulation into two major mechanisms. (A) **Activation of *Foxp3* transcription** is mainly regulated by TCR signals and enhanced by IL-2, TGF- β , and retinoic acid (RA). This may lead to thymic Treg selection and peripheral Treg differentiation. In addition, tonic TCR signals through self-reactive TCRs may use this mechanism to regulate homeostatic *Foxp3* transcription. (B) **Consolidation and tuning of *Foxp3* transcription.** The maintenance of *Foxp3* transcription requires CNS2

1 of the *Foxp3* gene, which may provide a platform for the Foxp3-Runx1/CBF- β
2 complex to form the autoregulatory transcriptional circuit (autoregulatory loop)
3 for the *Foxp3* gene. The activity of this loop can be affected by IL-2 signalling
4 via phosphorylated Stat5. This mechanism may lead to temporally-persistent
5 *Foxp3* transcription, which promotes effector Treg differentiation, and the
6 dynamic regulation of epigenetic modifications during Treg differentiation.

REFERENCES

1. Sakaguchi S, Yamaguchi T, Nomura T, Ono M. Regulatory T cells and immune tolerance. *Cell* 2008; **133**:775-87.
2. Josefowicz SZ, Lu LF, Rudensky AY. Regulatory T cells: mechanisms of differentiation and function. *Annu Rev Immunol* 2012; **30**:531-64.
3. Hsieh CS, Lee HM, Lio CW. Selection of regulatory T cells in the thymus. *Nat Rev Immunol* 2012; **12**:157-67.
4. Dujardin HC, Burlen-Defranoux O, Boucontet L, Vieira P, Cumano A, Bandeira A. Regulatory potential and control of Foxp3 expression in newborn CD4+ T cells. *Proc Natl Acad Sci U S A* 2004; **101**:14473-8.
5. Samy ET, Wheeler KM, Roper RJ, Teuscher C, Tung KS. Cutting edge: Autoimmune disease in day 3 thymectomized mice is actively controlled by endogenous disease-specific regulatory T cells. *Journal of immunology* 2008; **180**:4366-70.
6. Bailey-Bucktrout SL, Martinez-Llordella M, Zhou X, Anthony B, Rosenthal W, Luche H, Fehling HJ, Bluestone JA. Self-antigen-driven activation induces instability of regulatory T cells during an inflammatory autoimmune response. *Immunity* 2013; **39**:949-62.
7. Feng Y, Arvey A, Chinen T, van der Veen J, Gasteiger G, Rudensky AY. Control of the inheritance of regulatory T cell identity by a cis element in the Foxp3 locus. *Cell* 2014; **158**:749-63.
8. Beyersdorf N, Gaupp S, Balbach K, Schmidt J, Toyka KV, Lin C-H, Hanke T, Hünig T, Kerkau T, Gold R. Selective targeting of regulatory T cells with CD28 superagonists allows effective therapy of experimental autoimmune encephalomyelitis. *The Journal of Experimental Medicine* 2005; **202**:445-55.
9. Hünig T. The storm has cleared: lessons from the CD28 superagonist TGN1412 trial. *Nature Reviews Immunology* 2012; **12**:317.
10. Suntharalingam G, Perry MR, Ward S, Brett SJ, Castello-Cortes A, Brunner MD, Panoskaltsis N. Cytokine storm in a phase 1 trial of the anti-CD28 monoclonal antibody TGN1412. *N Engl J Med* 2006; **355**:1018-28.
11. Eastwood D, Findlay L, Poole S, Bird C, Wadhwa M, Moore M, Burns C, Thorpe R, Stebbings R. Monoclonal antibody TGN1412 trial failure explained by species differences in CD28 expression on CD4+ effector memory T-cells. *Br J Pharmacol* 2010; **161**:512-26.
12. Vitetta ES, Ghetie VF. Immunology. Considering therapeutic antibodies. *Science* 2006; **313**:308-9.
13. Zhou X, Bailey-Bucktrout S, Jeker LT, Bluestone JA. Plasticity of CD4(+) FoxP3(+) T cells. *Curr Opin Immunol* 2009; **21**:281-5.
14. Godfrey VL, Wilkinson JE, Russell LB. X-linked lymphoreticular disease in the scurfy (sf) mutant mouse. *Am J Pathol* 1991; **138**:1379-87.
15. Bennett CL, Christie J, Ramsdell F, Brunkow ME, Ferguson PJ, Whitesell L, Kelly TE, Saulsbury FT, Chance PF, Ochs HD. The immune dysregulation, polyendocrinopathy, enteropathy, X-linked syndrome (IPEX) is caused by mutations of FOXP3. *Nat Genet* 2001; **27**:20-1.
16. Tran DQ, Ramsey H, Shevach EM. Induction of FOXP3 expression in naive human CD4+FOXP3 T cells by T-cell receptor stimulation is transforming growth factor-beta dependent but does not confer a regulatory phenotype. *Blood* 2007; **110**:2983-90.
17. Miyao T, Floess S, Setoguchi R, Luche H, Fehling HJ, Waldmann H, Huehn J, Hori S. Plasticity of Foxp3(+) T cells reflects promiscuous Foxp3 expression in conventional T cells but not reprogramming of regulatory T cells. *Immunity* 2012; **36**:262-75.

- 1 18. Chen W, Jin W, Hardegen N, Lei KJ, Li L, Marinos N, McGrady G, Wahl SM. Conversion
2 of peripheral CD4+CD25- naive T cells to CD4+CD25+ regulatory T cells by TGF-beta
3 induction of transcription factor Foxp3. *J Exp Med* 2003; **198**:1875-86.
- 4 19. Ghiringhelli F, Puig PE, Roux S, Parcellier A, Schmitt E, Solary E, Kroemer G, Martin F,
5 Chauffert B, Zitvogel L. Tumor cells convert immature myeloid dendritic cells into TGF-
6 β -secreting cells inducing CD4+CD25+ regulatory T cell proliferation. *The Journal of*
7 *Experimental Medicine* 2005; **202**:919-29.
- 8 20. Huynh ML, Fadok VA, Henson PM. Phosphatidylserine-dependent ingestion of
9 apoptotic cells promotes TGF-beta1 secretion and the resolution of inflammation. *J*
10 *Clin Invest* 2002; **109**:41-50.
- 11 21. Malek TR. The biology of interleukin-2. *Annu Rev Immunol* 2008; **26**:453-79.
- 12 22. Miyara M, Yoshioka Y, Kitoh A, Shima T, Wing K, Niwa A, Parizot C, Taflin C, Heike T,
13 Valeyre D, Mathian A, Nakahata T, Yamaguchi T, Nomura T, Ono M, Amoura Z,
14 Gorochoy G, Sakaguchi S. Functional delineation and differentiation dynamics of
15 human CD4+ T cells expressing the FoxP3 transcription factor. *Immunity* 2009; **30**:899-
16 911.
- 17 23. Fujii H, Josse J, Tanioka M, Miyachi Y, Husson F, Ono M. Regulatory T Cells in
18 Melanoma Revisited by a Computational Clustering of FOXP3+ T Cell Subpopulations.
19 *Journal of immunology* 2016.
- 20 24. Seddiki N, Santner-Nanan B, Martinson J, Zaunders J, Sasson S, Landay A, Solomon M,
21 Selby W, Alexander SI, Nanan R, Kelleher A, Fazekas de St Groth B. Expression of
22 interleukin (IL)-2 and IL-7 receptors discriminates between human regulatory and
23 activated T cells. *J Exp Med* 2006; **203**:1693-700.
- 24 25. Liu W, Putnam AL, Xu-Yu Z, Szot GL, Lee MR, Zhu S, Gottlieb PA, Kapranov P, Gingeras
25 TR, Fazekas de St Groth B, Clayberger C, Soper DM, Ziegler SF, Bluestone JA. CD127
26 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T
27 reg cells. *J Exp Med* 2006; **203**:1701-11.
- 28 26. Bending D, Paduraru A, Ducker CB, Prieto Martín P, Crompton T, Ono M. A temporally
29 dynamic Foxp3 autoregulatory transcriptional circuit controls the effector Treg
30 programme. *The EMBO Journal* 2018.
- 31 27. Bending D, Martín PP, Paduraru A, Ducker C, Marzaganov E, Laviron M, Kitano S,
32 Miyachi H, Crompton T, Ono M. A timer for analyzing temporally dynamic changes in
33 transcription during differentiation in vivo. *The Journal of Cell Biology* 2018.
- 34 28. Fontenot JD, Rasmussen JP, Williams LM, Dooley JL, Farr AG, Rudensky AY. Regulatory
35 T cell lineage specification by the forkhead transcription factor foxp3. *Immunity* 2005;
36 **22**:329-41.
- 37 29. Haribhai D, Lin W, Relland LM, Truong N, Williams CB, Chatila TA. Regulatory T cells
38 dynamically control the primary immune response to foreign antigen. *Journal of*
39 *immunology* 2007; **178**:2961-72.
- 40 30. Rubtsov YP, Niec RE, Josefowicz S, Li L, Darce J, Mathis D, Benoist C, Rudensky AY.
41 Stability of the regulatory T cell lineage in vivo. *Science* 2010; **329**:1667-71.
- 42 31. Subach FV, Subach OM, Gundorov IS, Morozova KS, Piatkevich KD, Cuervo AM,
43 Verkhusha VV. Monomeric fluorescent timers that change color from blue to red
44 report on cellular trafficking. *Nat Chem Biol* 2009; **5**:118-26.
- 45 32. Zheng Y, Josefowicz S, Chaudhry A, Peng XP, Forbush K, Rudensky AY. Role of
46 conserved non-coding DNA elements in the Foxp3 gene in regulatory T-cell fate.
47 *Nature* 2010; **463**:808-12.
- 48 33. Floess S, Freyer J, Siewert C, Baron U, Olek S, Polansky J, Schlawe K, Chang HD, Bopp T,
49 Schmitt E, Klein-Hessling S, Serfling E, Hamann A, Huehn J. Epigenetic control of the
50 foxp3 locus in regulatory T cells. *PLoS Biol* 2007; **5**:e38.

- 1 34. Li X, Liang Y, LeBlanc M, Benner C, Zheng Y. Function of a Foxp3 cis-element in
2 protecting regulatory T cell identity. *Cell* 2014; **158**:734-48.
- 3 35. Levine AG, Arvey A, Jin W, Rudensky AY. Continuous requirement for the TCR in
4 regulatory T cell function. *Nature immunology* 2014; **15**:1070-8.
- 5 36. Vahl JC, Drees C, Heger K, Heink S, Fischer JC, Nedjic J, Ohkura N, Morikawa H, Poeck H,
6 Schallenberg S, Riess D, Hein MY, Buch T, Polic B, Schonle A, Zeiser R, Schmitt-Graff A,
7 Kretschmer K, Klein L, Korn T, Sakaguchi S, Schmidt-Supprian M. Continuous T cell
8 receptor signals maintain a functional regulatory T cell pool. *Immunity* 2014; **41**:722-
9 36.
- 10 37. Li MO, Rudensky AY. T cell receptor signalling in the control of regulatory T cell
11 differentiation and function. *Nat Rev Immunol* 2016; **16**:220-33.
- 12 38. Ono M, Tanaka RJ. Controversies concerning thymus-derived regulatory T cells:
13 fundamental issues and a new perspective. *Immunol Cell Biol* 2016; **94**:3-10.
- 14 39. Jordan MS, Boesteanu A, Reed AJ, Petrone AL, Hohenbeck AE, Lerman MA, Naji A,
15 Caton AJ. Thymic selection of CD4+CD25+ regulatory T cells induced by an agonist self-
16 peptide. *Nature immunology* 2001; **2**:301-6.
- 17 40. Bautista JL, Lio CW, Lathrop SK, Forbush K, Liang Y, Luo J, Rudensky AY, Hsieh CS.
18 Intracolon competition limits the fate determination of regulatory T cells in the
19 thymus. *Nature immunology* 2009; **10**:610-7.
- 20 41. Klein L, Kyewski B, Allen PM, Hogquist KA. Positive and negative selection of the T cell
21 repertoire: what thymocytes see (and don't see). *Nature Reviews Immunology* 2014;
22 **14**:377.
- 23 42. Itoh M, Takahashi T, Sakaguchi N, Kuniyasu Y, Shimizu J, Otsuka F, Sakaguchi S. Thymus
24 and autoimmunity: production of CD25+CD4+ naturally anergic and suppressive T cells
25 as a key function of the thymus in maintaining immunologic self-tolerance. *Journal of*
26 *immunology* 1999; **162**:5317-26.
- 27 43. Curotto de Lafaille MA, Lino AC, Kutchukhidze N, Lafaille JJ. CD25- T cells generate
28 CD25+Foxp3+ regulatory T cells by peripheral expansion. *Journal of immunology* 2004;
29 **173**:7259-68.
- 30 44. Moran AE, Holzapfel KL, Xing Y, Cunningham NR, Maltzman JS, Punt J, Hogquist KA. T
31 cell receptor signal strength in Treg and iNKT cell development demonstrated by a
32 novel fluorescent reporter mouse. *J Exp Med* 2011; **208**:1279-89.
- 33 45. McMurchy AN, Gillies J, Gizzi MC, Riba M, Garcia-Manteiga JM, Cittaro D, Lazarevic D,
34 Di Nunzio S, Piras IS, Bulfone A, Roncarolo MG, Stupka E, Bacchetta R, Levings MK. A
35 novel function for FOXP3 in humans: intrinsic regulation of conventional T cells. *Blood*
36 2013; **121**:1265-75.
- 37 46. Zheng Y, Manzotti CN, Burke F, Dussably L, Qureshi O, Walker LS, Sansom DM.
38 Acquisition of suppressive function by activated human CD4+ CD25- T cells is
39 associated with the expression of CTLA-4 not FoxP3. *Journal of immunology* 2008;
40 **181**:1683-91.
- 41 47. Mantel PY, Ouaked N, Ruckert B, Karagiannidis C, Welz R, Blaser K, Schmidt-Weber CB.
42 Molecular mechanisms underlying FOXP3 induction in human T cells. *Journal of*
43 *immunology* 2006; **176**:3593-602.
- 44 48. Isomura I, Palmer S, Grumont RJ, Bunting K, Hoyne G, Wilkinson N, Banerjee A,
45 Proietto A, Gugasyan R, Wu L, McNally A, Steptoe RJ, Thomas R, Shannon MF,
46 Gerondakis S. c-Rel is required for the development of thymic Foxp3+ CD4 regulatory T
47 cells. *J Exp Med* 2009; **206**:3001-14.
- 48 49. Long M, Park SG, Strickland I, Hayden MS, Ghosh S. Nuclear factor-kappaB modulates
49 regulatory T cell development by directly regulating expression of Foxp3 transcription
50 factor. *Immunity* 2009; **31**:921-31.

- 1 50. Ruan Q, Kameswaran V, Tone Y, Li L, Liou HC, Greene MI, Tone M, Chen YH.
2 Development of Foxp3(+) regulatory t cells is driven by the c-Rel enhanceosome.
3 Immunity 2009; **31**:932-40.
- 4 51. Kim HP, Leonard WJ. CREB/ATF-dependent T cell receptor-induced FoxP3 gene
5 expression: a role for DNA methylation. J Exp Med 2007; **204**:1543-51.
- 6 52. Sekiya T, Kashiwagi I, Yoshida R, Fukaya T, Morita R, Kimura A, Ichinose H, Metzger D,
7 Chambon P, Yoshimura A. Nr4a receptors are essential for thymic regulatory T cell
8 development and immune homeostasis. Nature immunology 2013; **14**:230-7.
- 9 53. Maira M, Martens C, Philips A, Drouin J. Heterodimerization between members of the
10 Nur subfamily of orphan nuclear receptors as a novel mechanism for gene activation.
11 Mol Cell Biol 1999; **19**:7549-57.
- 12 54. Duren RP, Boudreaux SP, Conneely OM. Genome Wide Mapping of NR4A Binding
13 Reveals Cooperativity with ETS Factors to Promote Epigenetic Activation of Distal
14 Enhancers in Acute Myeloid Leukemia Cells. PLoS One 2016; **11**:e0150450.
- 15 55. Sekiya T, Kashiwagi I, Inoue N, Morita R, Hori S, Waldmann H, Rudensky AY, Ichinose H,
16 Metzger D, Chambon P, Yoshimura A. The nuclear orphan receptor Nr4a2 induces
17 Foxp3 and regulates differentiation of CD4+ T cells. Nat Commun 2011; **2**:269.
- 18 56. Ono M, Tanaka RJ, Kano M. Visualisation of the T cell differentiation programme by
19 Canonical Correspondence Analysis of transcriptomes. BMC genomics 2014; **15**:1028.
- 20 57. Shimizu A, Kondo S, Sabe H, Ishida N, Honjo T. Structure and function of the interleukin
21 2 receptor: affinity conversion model. Immunol Rev 1986; **92**:103-20.
- 22 58. Gaffen SL. Signaling domains of the interleukin 2 receptor. Cytokine 2001; **14**:63-77.
- 23 59. Smith GA, Uchida K, Weiss A, Taunton J. Essential biphasic role for JAK3 catalytic
24 activity in IL-2 receptor signaling. Nature Chemical Biology 2016; **12**:373.
- 25 60. Sakaguchi S, Sakaguchi N, Asano M, Itoh M, Toda M. Immunologic self-tolerance
26 maintained by activated T cells expressing IL-2 receptor alpha-chains (CD25).
27 Breakdown of a single mechanism of self-tolerance causes various autoimmune
28 diseases. Journal of immunology 1995; **155**:1151-64.
- 29 61. Baecher-Allan C, Brown JA, Freeman GJ, Hafler DA. CD4+CD25high Regulatory Cells in
30 Human Peripheral Blood. The Journal of Immunology 2001; **167**:1245-53.
- 31 62. Burchill MA, Yang J, Vogtenhuber C, Blazar BR, Farrar MA. IL-2 receptor beta-
32 dependent STAT5 activation is required for the development of Foxp3+ regulatory T
33 cells. Journal of immunology 2007; **178**:280-90.
- 34 63. Yao Z, Kanno Y, Kerenyi M, Stephens G, Durant L, Watford WT, Laurence A, Robinson
35 GW, Shevach EM, Moriggl R, Hennighausen L, Wu C, O'Shea JJ. Nonredundant roles for
36 Stat5a/b in directly regulating Foxp3. Blood 2007; **109**:4368-75.
- 37 64. Fontenot JD, Rasmussen JP, Gavin MA, Rudensky AY. A function for interleukin 2 in
38 Foxp3-expressing regulatory T cells. Nature immunology 2005; **6**:1142-51.
- 39 65. Chinen T, Kannan AK, Levine AG, Fan X, Klein U, Zheng Y, Gasteiger G, Feng Y, Fontenot
40 JD, Rudensky AY. An essential role for the IL-2 receptor in Treg cell function. Nature
41 immunology 2016; **17**:1322-33.
- 42 66. Antov A, Yang L, Vig M, Baltimore D, Van Parijs L. Essential Role for STAT5 Signaling in
43 CD25+CD4+ Regulatory T Cell Homeostasis and the Maintenance of Self-Tolerance. The
44 Journal of Immunology 2003; **171**:3435-41.
- 45 67. Snow JW, Abraham N, Ma MC, Herndier BG, Pastuszak AW, Goldsmith MA. Loss of
46 Tolerance and Autoimmunity Affecting Multiple Organs in STAT5A/5B-Deficient Mice.
47 The Journal of Immunology 2003; **171**:5042-50.
- 48 68. Feinerman O, Jentsch G, Tkach KE, Coward JW, Hathorn MM, Sneddon MW, Emonet T,
49 Smith KA, Altan-Bonnet G. Single-cell quantification of IL-2 response by effector and

- regulatory T cells reveals critical plasticity in immune response. *Mol Syst Biol* 2010; **6**:437.
69. Massagué J. TGF β signalling in context. *Nature Reviews Molecular Cell Biology* 2012; **13**:616.
70. Oh SA, Li MO. TGF- β : Guardian of T Cell Function. *The Journal of Immunology* 2013; **191**:3973-9.
71. Bettelli E, Carrier Y, Gao W, Korn T, Strom TB, Oukka M, Weiner HL, Kuchroo VK. Reciprocal developmental pathways for the generation of pathogenic effector TH17 and regulatory T cells. *Nature* 2006; **441**:235-8.
72. Laurence A, Tato CM, Davidson TS, Kanno Y, Chen Z, Yao Z, Blank RB, Meylan F, Siegel R, Hennighausen L, Shevach EM, O'Shea JJ. Interleukin-2 signaling via STAT5 constrains T helper 17 cell generation. *Immunity* 2007; **26**:371-81.
73. Tone Y, Furuuchi K, Kojima Y, Tykocinski ML, Greene MI, Tone M. Smad3 and NFAT cooperate to induce Foxp3 expression through its enhancer. *Nature immunology* 2007; **9**:194.
74. Schlenner SM, Weigmann B, Ruan Q, Chen Y, von Boehmer H. Smad3 binding to the foxp3 enhancer is dispensable for the development of regulatory T cells with the exception of the gut. *J Exp Med* 2012; **209**:1529-35.
75. Durant L, Watford WT, Ramos HL, Laurence A, Vahedi G, Wei L, Takahashi H, Sun HW, Kanno Y, Powrie F, O'Shea JJ. Diverse targets of the transcription factor STAT3 contribute to T cell pathogenicity and homeostasis. *Immunity* 2010; **32**:605-15.
76. Veldhoen M, Stockinger B. TGF β 1, a Jack of all trades;: the link with pro-inflammatory IL-17-producing T cells. *Trends in Immunology* 2006; **27**:358-61.
77. Evans HG, Gullick NJ, Kelly S, Pitzalis C, Lord GM, Kirkham BW, Taams LS. In vivo activated monocytes from the site of inflammation in humans specifically promote Th17 responses. *Proc Natl Acad Sci U S A* 2009; **106**:6232-7.
78. Kitoh A, Ono M, Naoe Y, Ohkura N, Yamaguchi T, Yaguchi H, Kitabayashi I, Tsukada T, Nomura T, Miyachi Y, Taniuchi I, Sakaguchi S. Indispensable role of the Runx1-Cbfbeta transcription complex for in vivo-suppressive function of FoxP3+ regulatory T cells. *Immunity* 2009; **31**:609-20.
79. Ono M, Yaguchi H, Ohkura N, Kitabayashi I, Nagamura Y, Nomura T, Miyachi Y, Tsukada T, Sakaguchi S. Foxp3 controls regulatory T-cell function by interacting with AML1/Runx1. *Nature* 2007; **446**:685-9.
80. Rudra D, Egawa T, Chong MM, Treuting P, Littman DR, Rudensky AY. Runx-CBfbeta complexes control expression of the transcription factor Foxp3 in regulatory T cells. *Nature immunology* 2009; **10**:1170-7.
81. Bruno L, Mazzearella L, Hoogenkamp M, Hertweck A, Cobb BS, Sauer S, Hadjur S, Leleu M, Naoe Y, Telfer JC, Bonifer C, Taniuchi I, Fisher AG, Merckenschlager M. Runx proteins regulate Foxp3 expression. *The Journal of Experimental Medicine* 2009; **206**:2329-37.
82. Polansky JK, Schreiber L, Thelemann C, Ludwig L, Kruger M, Baumgrass R, Cording S, Floess S, Hamann A, Huehn J. Methylation matters: binding of Ets-1 to the demethylated Foxp3 gene contributes to the stabilization of Foxp3 expression in regulatory T cells. *J Mol Med (Berl)* 2010; **88**:1029-40.
83. Shrivastava T, Mino K, Babayeva ND, Baranovskaya OI, Rizzino A, Tahirov TH. Structural basis of Ets1 activation by Runx1. *Leukemia* 2014; **28**:2040-8.
84. Bending D, Giannakopoulou E, Lom H, Wedderburn LR. Synovial Regulatory T Cells Occupy a Discrete TCR Niche in Human Arthritis and Require Local Signals To Stabilize FOXP3 Protein Expression. *Journal of immunology* 2015; **195**:5616-24.

85. Dias S, D'Amico A, Cretney E, Liao Y, Tellier J, Bruggeman C, Almeida FF, Leahy J, Belz GT, Smyth GK, Shi W, Nutt SL. Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. *Immunity* 2017; **46**:78-91.
86. Liu B, Tahk S, Yee KM, Fan G, Shuai K. The ligase PIAS1 restricts natural regulatory T cell differentiation by epigenetic repression. *Science* 2010; **330**:521-5.
87. Josefowicz SZ, Wilson CB, Rudensky AY. Cutting edge: TCR stimulation is sufficient for induction of Foxp3 expression in the absence of DNA methyltransferase 1. *Journal of immunology* 2009; **182**:6648-52.
88. Xing S, Li F, Zeng Z, Zhao Y, Yu S, Shan Q, Li Y, Phillips FC, Maina PK, Qi HH, Liu C, Zhu J, Pope RM, Musselman CA, Zeng C, Peng W, Xue HH. Tcf1 and Lef1 transcription factors establish CD8(+) T cell identity through intrinsic HDAC activity. *Nature immunology* 2016; **17**:695-703.
89. Li C, Ebert PJR, Li Q-J. T Cell Receptor (TCR) and Transforming Growth Factor β (TGF- β) Signaling Converge on DNA (Cytosine-5)-methyltransferase to Control forkhead box protein 3 (foxp3) Locus Methylation and Inducible Regulatory T Cell Differentiation. *Journal of Biological Chemistry* 2013; **288**:19127-39.
90. Toker A, Engelbert D, Garg G, Polansky JK, Floess S, Miyao T, Baron U, Duber S, Geffers R, Giehr P, Schallenberg S, Kretschmer K, Olek S, Walter J, Weiss S, Hori S, Hamann A, Huehn J. Active demethylation of the Foxp3 locus leads to the generation of stable regulatory T cells within the thymus. *Journal of immunology* 2013; **190**:3180-8.
91. Placek K, Hu G, Cui K, Zhang D, Ding Y, Lee JE, Jang Y, Wang C, Konkel JE, Song J, Liu C, Ge K, Chen W, Zhao K. MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. *Nature immunology* 2017; **18**:1035-45.
92. Kitagawa Y, Ohkura N, Kidani Y, Vandenbon A, Hirota K, Kawakami R, Yasuda K, Motooka D, Nakamura S, Kondo M, Taniuchi I, Kohwi-Shigematsu T, Sakaguchi S. Guidance of regulatory T cell development by Satb1-dependent super-enhancer establishment. *Nature immunology* 2016; **18**:173.
93. Delacher M, Imbusch CD, Weichenhan D, Breiling A, Hotz-Wagenblatt A, Trager U, Hofer AC, Kagebein D, Wang Q, Frauhammer F, Mallm JP, Bauer K, Herrmann C, Lang PA, Brors B, Plass C, Feuerer M. Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. *Nature immunology* 2017; **18**:1160-72.
94. Zemmour D, Zilionis R, Kiner E, Klein AM, Mathis D, Benoist C. Single-cell gene expression reveals a landscape of regulatory T cell phenotypes shaped by the TCR. *Nature immunology* 2018; **19**:291-301.
95. Weiss JM, Bilate AM, Gobert M, Ding Y, Curotto de Lafaille MA, Parkhurst CN, Xiong H, Dolpady J, Frey AB, Ruocco MG, Yang Y, Floess S, Huehn J, Oh S, Li MO, Niec RE, Rudensky AY, Dustin ML, Littman DR, Lafaille JJ. Neuropilin 1 is expressed on thymus-derived natural regulatory T cells, but not mucosa-generated induced Foxp3+ T reg cells. *J Exp Med* 2012; **209**:1723-42, S1.
96. Thornton AM, Korty PE, Tran DQ, Wohlfert EA, Murray PE, Belkaid Y, Shevach EM. Expression of Helios, an Ikaros transcription factor family member, differentiates thymic-derived from peripherally induced Foxp3+ T regulatory cells. *Journal of immunology* 2010; **184**:3433-41.
97. Szurek E, Cebula A, Wojciech L, Pietrzak M, Rempala G, Kisielow P, Ignatowicz L. Differences in Expression Level of Helios and Neuropilin-1 Do Not Distinguish Thymus-Derived from Extrathymically-Induced CD4+Foxp3+ Regulatory T Cells. *PLoS One* 2015; **10**:e0141161.